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Identification Of MicroRNAs In Normal And Mantled Oil Palm Fruit via 454 Transcriptome Sequencing

Chatchawan Jantasuriyarat[1] , Sithichoke Tangphatsornruang[2] , Jittima Piriyapongsa[2] , Chatree Saensuk[3] , Apichart Vanavichit[3] , Timothy J. Tranbarger[4] , Morcillo Fabienne[5] , Somvong Tragoonrung[2]

[1] Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, 10900 Thailand
[2] Genome Institute, BIOTEC, Klong Luang, Pathumthani 12120, Thailand
[3] Rice Gene Discovery Unit, Kasetsart University, Kamphaeng Sean Campus, Nakhon Pathom 73140, Thailand
[4] Institut de Recherche pour le Developpement, UMR DIAPC, Palm Development Group, France
[5] Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement, CIRAD, UMR DAP, PHIV, France

Small RNAs such as miRNAs and siRNAs play a critical role in post-transcriptional gene regulation and have been shown to control many genes involved in various biological processes including fruit development. Oil palm (Elaeis guineensis Jacq) belongs to the Arecaceae family and is the number one source of edible vegetable oil worldwide. Abnormality of oil palm fruit (mantled) caused by the tissue culture process produces a low oil bearing fruit. Deep sequencing of the small RNA component of the normal and mantled oil palm fruit transcriptome is an important step toward understanding the mechanisms of small RNAs on fruit development in oil palm. The current project focuses on applying 454 pyrosequencing technology to sequence small RNAs from normal and mantled oil palm fruit. A total of 86,090 reads (7,863,568 bp) were obtained from normal and mantled female flower libraries (with 53,487 and 32,603 reads respectively). The reads length ranged from 40 bp to 540 bp with an average length of 90 bp. Based on sequence similarity and hairpin structure prediction, we found 121 reads perfectly matched to 31 known sequences of highly conserved plant miRNA families. The identification of novel miRNA candidates are in progress and the confirmation of conserved and novel miRNA by qRT-PCR analysis will be presented.